In the Claims

Please amend the claims as follows:

1-51 (Cancelled)

52. (New) A method of comparing one or more single-stranded nucleic acid targets within two or more samples, comprising:

a) obtaining at least a first sample and a second sample, each potentially having at least a first nucleic acid target;

b) preparing at least a first tagged nucleic acid sample by appending at least a first nucleic acid tag comprising a first amplification domain and a first differentiation domain to the first nucleic acid target of the first sample, if the first nucleic acid target is present in the first sample;

c) preparing at least a second tagged nucleic acid sample by appending at least a second nucleic acid tag comprising a second amplification domain and a second differentiation domain to the first nucleic acid target of the second sample, if the first nucleic acid target is present in the second sample;

d) mixing the first tagged nucleic acid sample and the second tagged nucleic acid sample to create a sample mixture;

e) co-amplifying said first nucleic acid target of the first sample and said first nucleic acid target of the second sample in the sample mixture, if both the first and second nucleic acid targets are present in the sample mixture, wherein said co-amplifying produces at least a first amplified nucleic acid comprising at least the first differentiation domain and a segment of the target nucleic acid from the first sample, if the first nucleic acid target is present in the first sample, and at least a second amplified nucleic acid comprising at least the second differentiation domain and a segment of the target nucleic acid from

the second sample, if the first nucleic acid target is present in the second sample;

f) differentiating the first amplified nucleic acid, if any, from the second amplified nucleic acid, if any; and

g) comparing abundance of the differentiated nucleic acid from the first nucleic acid target of said first sample to abundance of the differentiated nucleic acid from the first nucleic acid target of said second sample.

53. (New) The method of claim 52, wherein the differentiation domain of the first tag and the second tag is appended between the first nucleic acid target sequence and the amplification domain.

54. (New) The method of claim 52, wherein the differentiation domain of the first nucleic acid tag and the second nucleic acid tag comprise at least a primer binding domain, a transcription domain, a size differentiation domain, an affinity domain, a unique sequence domain, or a restriction enzyme domain.

55. (New) The method of claim 52, wherein differentiating comprises production of at least one differentiated nucleic acid from said first or second amplified nucleic acid.

56. (New) The method of claim 55, wherein said differentiated nucleic acid is labeled.

57. (New) The method of claims 52, wherein the first nucleic acid tag or second nucleic acid tag further comprises at least one additional domain.

58. (New) The method of claim 57, wherein the additional domain is a labeling domain, a restriction enzyme domain, a secondary amplification domain, a secondary fingerprint domain or a combination thereof.

59. (New) The method of claims 52, wherein said nucleic acid target is one target of a plurality of nucleic acid targets within the samples.

60. (New) The method of claims 52, wherein said first and second sample are two samples of a plurality of samples.

61. (New) The method of claim 60, wherein the first and second tag are two tags of a plurality of tags.

62. (New) The method of claim 52, wherein said differentiation domains of the first nucleic acid tag and the second nucleic acid tag are affinity domains.

63. (New) The method of claim 62, wherein differentiating comprises binding at least a first ligand to at least a segment of the affinity domain.

64. (New) The method of claim 63, wherein the first ligand comprises a nucleic acid, protein, or other molecule with affinity for certain nucleic acids.

65. (New) The method of claim 65, wherein the first ligand is used to separate the first target nucleic acid from at least one other nucleic acid or molecule.

66. (New) The method of claims 65, wherein the first ligand is bound to at least one solid support.

67. (New) The method of claim 66, wherein the solid support is an array, a chip, a membrane, a bead, a glass slide, or a microtiter well, or a combination thereof.

68. (New) The method of claim 52, wherein said differentiation domains of the first and second nucleic acids are unique sequence domains.

69. (New) The method of claim 68, wherein differentiating comprises sequencing through the differentiation domains of the amplified nucleic acids.

70. (New) The method of claim 52, wherein the differentiation domains of the first nucleic acid tag and the second nucleic acid tag each comprise at least one transcription domain.

71. (New) The method of claim 70, wherein differentiating comprises a transcription reaction.

72. (New) The method of claim 71, wherein said transcription reaction produces at least one differentiated nucleic acid.

73. (New) The method of claim 72, wherein said differentiated nucleic acid includes a detectable moiety.

74. (New) The method of claim 52, wherein the differentiation domain of the first nucleic acid tag and the second nucleic acid tag each comprise at least one size differentiation domain.

75. (New) The method of claim 74, wherein said differentiating comprises distinguishing the amplification products from the first and second samples by size.

76. (New) The method of claim 52, wherein said differentiation domain of the first nucleic acid tag or the second nucleic acid tag comprises at least one restriction enzyme cleavage domain.

77. (New) The method of claim 76, further comprising cleaving said restriction enzyme cleavage site to promote the ligation of a label or at least one additional domain to a segment of the at least a first or at least a second nucleic acid tag.

78. (New) The method of claim 76, wherein differentiating comprises cleaving said restriction enzyme site to remove at least one label.

79. (New) The method of claim 52, further comprising isolating at least a first target fraction of the sample mixture prior to amplification.

80. (New) The method of claim 52, wherein the amplification domain of the first nucleic acid tag and the second nucleic acid tag comprises a primer binding domain.

81. (New) The method of claims 80, further comprising at least one primer extension reaction.

82. (New) The method of claim 52, wherein the amplification domain of the first nucleic acid tag and the second nucleic acid tag comprises a transcription domain.

83. (New) The method of claim 52, wherein the amplification domains of the first and second nucleic acid tags are functionally equivalent.

84. (New) The method of claim 83, wherein the amplification domains of the first and second nucleic acid tags are identical.

85. (New) The method of claim 79, wherein said first target fraction is one of a plurality of target fractions.

86. (New) The method of claim 79, wherein the first target fraction is isolated by binding a ligand to at least a segment of the first nucleic acid target.

87. (New) The method of claim 86, wherein the ligand is a nucleic acid, protein, or other molecule with an affinity for certain nucleic acids.

88. (New) The method of claim 87, wherein the ligand is a nucleic acid complementary to at least a segment of the first nucleic acid target.

89. (New) The method of claim 88, wherein the first complementary nucleic acid is used to separate the first target nucleic acid from at least one other nucleic acid or molecule.

90. (New) The method of claim 89, wherein the target fraction is subsequently removed from the first complementary nucleic acid.

91. (New) The method of claim 88, wherein the first complementary nucleic acid is one of a plurality of complementary nucleic acids, and each complementary nucleic acid is complementary to one of a plurality of nucleic acid targets.

92. (New) The method of claim 88, wherein the first complementary nucleic acid is bound to a solid support.

93. (New) The method of claim 92, wherein the first complementary nucleic acid is one of a plurality of complementary acids bound to an array, and each of the complementary nucleic acids is complementary to one of a plurality of nucleic acid targets.

94. (New) The method of claim 92, wherein the solid support is one of a plurality of solid supports.

95. (New) The method of claim 92, wherein the solid support is an array, a microtiter well, a chip, a bead or a combination thereof.

96. (New) The method of claim 52, wherein said differentiation domain of the first nucleic acid tag comprises a first affinity domain and the second nucleic acid tag comprises a second affinity domain that is distinct from the first affinity domain.

97. (New) The method of claim 96, wherein differentiating comprises binding at least a segment of the first affinity domain to a first affinity domain specific ligand and/or binding at least a segment of the second affinity domain to a second affinity domain specific ligand.

98. (New) The method of claim 97, wherein the first and second affinity domain specific ligands are two of a plurality of ligands.

99. (New) The method of claim 97, wherein at least one of the first or the second affinity domain specific ligands is bound to at least one solid support.

100. (New) The method of claim 79, wherein differentiating comprises sequencing the first amplified nucleic acid and the second amplified nucleic acid.

101. (New) The method of claim 98, wherein said additional domain is a restriction enzyme domain, a secondary amplification domain, a secondary differentiation domain, a sequencing primer binding domain, a labeling domain or a combination thereof.

102. (New) The method of claim 52, further comprising

h) adding a limiting concentration of at least a first target specific primer to the sample mixture; and,

i) processing the sample mixture by a process comprising at least a first extension reaction to produce a limited concentration of first product nucleic acids complementary to the first nucleic acid target of the first sample, if the first nucleic acid target is present in the first sample, and a limited concentration of second product nucleic acids complementary to the first nucleic acid target of the second sample, if the first nucleic acid target is present in the second sample, wherein any first product nucleic acids comprise the first differentiation domain and a section of the first nucleic acid target from the first sample and any second product nucleic acids comprise the second differentiation domain and a section of the first nucleic acid target from the second sample.

103. (New) The method of claim 52, wherein the first differentiation domain is a first fingerprint domain and the second differentiation domain is a second fingerprint domain and wherein amplifying the first nucleic acid target uses at least one adapter primer or arbitrary primer specific to a subset of the nucleic acid in the first sample and one primer specific to the

amplification domain, and wherein differentiating the first amplified nucleic acid in f) comprises generating labeled nucleic acid from the first amplified nucleic acid using the finger print domain.

104. (New) The method of claim 103, wherein comparing abundance of the differentiated nucleic acid comprises fractionating the labeled nucleic acid to create a fingerprint of the sample.

105. (New) A method of comparing one or more nucleic acid targets within two or more samples, comprising:

a) obtaining at least a first sample and a second sample, each potentially having at least a first nucleic acid target;

b) preparing at least a first tagged nucleic acid sample by appending at least a first nucleic acid tag comprising a first amplification domain and a first differentiation domain to the first nucleic acid target of the first sample, if the first nucleic acid target is present in the first sample;

c) preparing at least a second tagged nucleic acid sample by appending at least a second nucleic acid tag comprising a second amplification domain and a second differentiation domain to the first nucleic acid target of the second sample, if the first nucleic acid target is present in the second sample;

d) mixing the first tagged nucleic acid sample and the second tagged nucleic acid sample to create a sample mixture;

e) isolating at least a first target fraction of the sample mixture;

f) performing at least a first amplification reaction on the first target fraction, wherein the amplification reaction produces at least a first amplified nucleic acid comprising the first differentiation domain and a segment of the first nucleic acid

target, if the first nucleic acid target is present in the first sample, and at least a second amplified nucleic acid comprising the second differentiation domain and a segment of the first nucleic acid target, if the first nucleic acid target is present in the second sample;

g) differentiating the first amplified nucleic acid in the first target fraction, if any, from the second amplified nucleic acid in the first target fraction, if any; and

h) comparing the first nucleic acid target of said first sample to the nucleic acid target of said second sample.

106. (New) The method of claim 105, wherein the differentiation domain of the first nucleic acid tag and the second nucleic acid tag comprise at least a size differentiation domain, an affinity domain, or a unique sequence domain.

107. (New) The method of claim 105, wherein the first target fraction is isolated by binding a ligand to at least a segment of the first nucleic acid target.

108. (New) A method for comparing one or more nucleic acid targets within two or more samples comprising:

a) obtaining at least a first sample and a second sample, each potentially having at least a first nucleic acid target;

b) preparing at least a first tagged nucleic acid sample by appending at least a first nucleic acid tag comprising a first differentiation domain to the first nucleic acid target of the first sample, if the first nucleic acid target is present in the first sample;

c) preparing at least a second tagged nucleic acid sample by appending at least a second nucleic acid tag comprising a second differentiation domain to the first nucleic

acid target of the second sample, if the first nucleic acid target is present in the second sample;

d) mixing the first tagged nucleic acid sample and the second tagged nucleic acid sample to create a sample mixture;

e) adding a limiting concentration of at least a first target specific primer to the sample mixture;

f) processing the sample mixture by a process comprising at least a first extension reaction to produce a limited concentration of first product nucleic acids complementary to the first nucleic acid target of the first sample, if the first nucleic acid target is present in the first sample, and a limited concentration of second product nucleic acids complementary to the first nucleic acid target of the second sample, if the first nucleic acid target is present in the second sample, wherein any first product nucleic acids comprise the first differentiation domain and a section of the first nucleic acid target from the first sample and any second product nucleic acids comprise the second differentiation domain and a section of the first nucleic acid target from the second sample;

g) differentiating any first product nucleic acids from any second product nucleic acids; and

h) comparing the amount of first nucleic acid target in the first sample, if any, to the amount of first nucleic acid target of the second sample, if any.

109. (New) The method of claim 108, wherein the processing of the sample mixture further comprises amplification to produce amplified nucleic acid from the first sample and amplified nucleic acid from the second sample.

110. (New) The method of claim 109, wherein the amplification process comprises a plurality of primer extension reactions.

111. (New) The method of claim 108, wherein a non-limiting amount of a primer specific to the amplification domains and a limited amount of a primer specific to the first target are added to the sample mixture and the processing of the sample mixture comprises multiple cycles of primer extension to produce a limited concentration of first product nucleic acids complementary to the first nucleic acid target of the first sample, if the first nucleic acid target is present in the first sample, and a limited concentration of second product nucleic acids complementary to the first nucleic acid target of the second sample, if the first nucleic acid target is present in the second sample.

112. (New) The method of claim 108, wherein the differentiation domain of the first nucleic acid tag or the second nucleic acid tag comprises a primer binding domain, a transcription domain, an affinity domain, a restriction enzyme cleavage domain, or a combination thereof.

113. (New) A method of analyzing one or more samples comprising:

a) obtaining a first sample;

b) preparing at least a first tagged nucleic acid sample by appending to at least a first nucleic acid target of the first sample at least a first nucleic acid tag, the nucleic acid tag comprising an amplification domain and a fingerprint domain;

c) amplifying the nucleic acid target using at least one adapter primer or arbitrary primer specific to a subset of the nucleic acid in the sample and one primer specific to the amplification domain, to produce at least a first amplified nucleic acid comprising the fingerprint domain and a segment of the first nucleic acid target;

d) generating labeled nucleic acid from the first amplified nucleic acid using the fingerprint domain; and

e) fractionating the labeled nucleic acid to create a fingerprint of the sample.

114. (New) The method of claim 113, wherein the first nucleic acid tag is appended to a target nucleic acid in each of the plurality of samples to prepare a plurality of tagged nucleic acid samples and each tagged nucleic acid sample is amplified in a separate reaction.

115. (New) The method of claim 113 further defined as comprising:

a) obtaining a plurality of samples;

b) preparing a plurality of tagged nucleic acid samples by appending to at least the first nucleic acid target in each of the plurality of samples a plurality of nucleic acid tags, each nucleic acid tag comprising the amplification domain and a fingerprint domain, wherein the fingerprint domain for each sample is unique to that sample;

c) mixing the plurality of tagged nucleic acid samples to create a mixture of tagged nucleic acid samples;

d) amplifying the first nucleic acid target in the mixture, using at least one arbitrary primer or adaptor primer and one primer specific to the amplification domain, to produce amplified nucleic acid comprising a plurality of amplified nucleic acids, each of which comprises a fingerprint domain and a segment of the first nucleic acid target;

e) separating the amplified nucleic acid into a plurality of aliquots;

f) generating labeled nucleic acid from each aliquot using a fingerprint domain unique to a different sample for each aliquot; and

g) fractionating the labeled nucleic acid from each aliquot to create a plurality of fingerprints.

116. (New) The method of claim 113, wherein the fingerprint domain of the first nucleic acid tag or the second nucleic acid tag comprises a primer binding domain, a transcription domain, an affinity domain, or a combination thereof.